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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Fri Aug 03 11:07:58 EDT 2007

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Reviewer Comments:

10583785 errors

<210> 6

<211> 1671

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of human SP-B precursor lacking the C-terminal
propeptide

<220>

<221> CDS

<222> (844) ... (1671)

<223> Coding sequence of low mw two-chain urokinase-plasminogen activator

What about locations 838 through 843? They are not explained. This type of error also appears in Sequences 7, 12, 13, 19, 20, 25, and 26. See below for another error in Sequence 19.

<210> 19

<211> 557

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE
<222> (1) ... (279)
<223> Human surfactant protein B precursor lacking the C-terminal
propeptide

<220>

<221> PEPTIDE
<222> (282) ... (577)
<223> Human low molecular weight two-chain urokinase-plasminogen
activator

Not only are locations 280 through 281 not explained, but the above
<222> response is incorrect. It states <222> (282) ... (577); however,
only 557 amino acids are in the sequence.

<400> 26

Met	Arg	Ala	Leu	Leu	Ala	Arg	Leu	Leu	Leu	Cys	Val	Leu	Val	Val	Ser
1				5					10					15	

Asp	Ser	Lys	Gly	Ser	Asn	Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	Leu	Lys
				20					25					30	

Please delete the blank line between the above amino acids and their
numbering.

Application No: 10583785 Version No: 3.0

Input Set:**Output Set:**

Started: 2007-07-24 12:08:44.453
Finished: 2007-07-24 12:08:47.371
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 918 ms
Total Warnings: 8
Total Errors: 10
No. of SeqIDs Defined: 26
Actual SeqID Count: 26

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (26)

Input Set:

Output Set:

Started: 2007-07-24 12:08:44.453
Finished: 2007-07-24 12:08:47.371
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 918 ms
Total Warnings: 8
Total Errors: 10
No. of SeqIDs Defined: 26
Actual SeqID Count: 26

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)

SEQUENCE LISTING

<110> Werner Seeger

<120> Novel Chimeric Plasminogen Activators and Their Pharmaceutical Use

<130> 607927-000001

<140> 10583785

<141> 2007-07-24

<150> US/10/583,785

<151> 2006-06-19

<160> 26

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1143)

<223> Coding sequence of the surfactant protein B precursor

<400> 1

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg 48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
1 5 10 15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt 96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
20 25 30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag 144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
35 40 45

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga 192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
50 55 60

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac 240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
65 70 75 80

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg 288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
85 90 95

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc 336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
100 105 110

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag 384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
115 120 125

aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	
195 200 205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag	672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
210 215 220	
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg	720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225 230 235 240	
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc	768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	
245 250 255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
260 265 270	
ctc gtc ctc cgg tgc tcc atg gat gac agc gct ggc cca agg tcg ccg	864
Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro	
275 280 285	
aca gga gaa tgg ctg ccg cga gac tct gag tgc cac ctc tgc atg tcc	912
Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser	
290 295 300	
gtg acc acc cag gcc ggg aac agc agc gag cag gcc ata cca cag gca	960
Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala	
305 310 315 320	
atg ctc cag gcc tgt gtt ggc tcc tgg ctg gac agg gaa aag tgc aag	1008
Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys	
325 330 335	
caa ttt gtg gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg	1056
Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg	
340 345 350	

ggc tgg gat gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc 1104
Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr
355 360 365

atg tcc agc cct ctc cag tgt atc cac agc ccc gac ctt 1143
Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu
370 375 380

<210> 2

<211> 837

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of SP-B precursor lacking the C-terminal propeptide

<400> 2

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg 48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
1 5 10 15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt 96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
20 25 30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag 144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
35 40 45

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga 192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
50 55 60

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac 240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
65 70 75 80

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg 288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
85 90 95

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc 336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
100 105 110

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag 384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
115 120 125

aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa 432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
130 135 140

tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg 480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
145 150 155 160

ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc 528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
165 170 175

gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac 576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
180 185 190

aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc 624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
195 200 205

tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag 672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
210 215 220

ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg 720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
225 230 235 240

gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc 768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
245 250 255

ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc 816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
260 265 270

ctc gtc ctc cgg tgc tcc atg 837
Leu Val Leu Arg Cys Ser Met
275

<210> 3
<211> 237
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (237)
<223> Coding sequence of the mature surfactant protein B

<400> 3

ttc ccc att cct ctc ccc tat tgc tgg ctc tgc agg gct ctg atc aag 48
Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys
1 5 10 15

cgg atc caa gcc atg att ccc aag ggt gcg cta gct gtg gca gtg gcc 96
Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala
20 25 30

cag gtg tgc cgc gtg gta cct ctg gtg gcg ggc ggc atc tgc cag tgc 144
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys
35 40 45

ctg gct gag cgc tac tcc gtc atc ctg ctc gac acg ctg ctg ggc cgc 192
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg
50 55 60

atg ctg ccc cag ctg gtc tgc cgc ctc gtc ctc cgg tgc tcc atg 237
Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met
65 70 75

<210> 4

<211> 1293

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1293)

<223> Coding sequence of the single-chain urokinase-plasminogen activator

<400> 4

atg aga gcc ctg ctg gcg cgc ctg ctt ctc tgc gtc ctg gtc gtg agc 48
Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1 5 10 15

gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac 96
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
20 25 30

tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att 144
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
35 40 45

cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata 192
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
50 55 60

gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga 240
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65 70 75 80

aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct 288
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
85 90 95

gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt 336
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
100 105 110

cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg 384
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
115 120 125

agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa	432
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln	
130 135 140	
gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct	480
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro	
145 150 155 160	
cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc	528
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg	
165 170 175	
ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg	576
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp	
180 185 190	
ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg	624
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val	
195 200 205	
tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac	672
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His	
210 215 220	
tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt	720
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly	
225 230 235 240	
cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg	768
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val	
245 250 255	
gaa aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac	816
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His	
260 265 270	
cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt	864
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys	
275 280 285	
gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat	912
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr	
290 295 300	
aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa	960
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys	
305 310 315 320	
gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt	1008
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val	
325 330 335	
gtg aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc	1056
Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly	
340 345 350	
tct gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa	1104

Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys
355 360 365

aca gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc 1152
Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu
370 375 380

caa ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt 1200
Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
385 390 395 400

gcc ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta 1248
Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
405 410 415

ccc tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc 1293
Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu
420 425 430

<210> 5
<211> 828
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (828)
<223> Coding sequence of low mw two-chain urokinase-plasminogen activator

<400> 5

aag ccc tcc tct cct cca gaa gaa tta aaa ttt cag tgt ggc caa aag 48
Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys
1 5 10 15

act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc 96
Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile
20 25 30

gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc 144
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly
35 40 45

tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg 192
Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val
50 55 60

atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac 240
Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr
65 70 75 80

atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag 288
Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu
85 90 95

atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct	336
Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala	
100 105 110	
gac acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc	384
Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser	
115 120 125	
aag gag ggc agg tgt gcg cag cca tcc cgg act ata cag acc atc tgc	432
Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys	
130 135 140	
ctg ccc tcg atg tat aac gat ccc cag ttt ggc aca agc tgt gag atc	480
Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile	
145 150 155 160	
act ggc ttt gga aaa gag aat tct acc gac tat ctc tat ccg gag cag	528
Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln	
165 170 175	
ctg aaa atg act gtt gtg aag ctg att tcc cac cgg gag tgt cag cag	576
Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln	
180 185 1	